



Docket No.: CL001187
Serial No.: 09/817,199
Inventors: SHAO, Wei et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

```
1 TTCGCCTGCG GGCCGGCACT GCTCACCTCT CGTCCAGGGA CATGACGGGC
51 ACGCCAGGCG CCGTTGCCAC CCGGGATGGC GAGGCCCCCG AGCGCTCCCC
101 GCCCTGCACT CCGAGCTACG ACCTCACGGG CAAGGTGATG CTTCTGGGAG
151 ACACAGGCGT CGGCAAAACA TGTTTCCTGA TCCAAATCAA AGACGGGGCC
201 TTCCTGTCCG GAACCTTCAT AGCCACCGTC GGCATAGACT TCAGGAACAA
251 GGTGGTGACT GTGGATGGCG TGAGAGTGAA GCTGCAGATC TGGGACACCG
301 CTGGGCAGGA ACGGTTCCGA AGCGTCACCC ATGCTTATTA CAGAGATGCT
351 CAGGCCTTGC TTCTGCTGTA TGACATCACC AACAAATCTT CTTTCGACAA
401 CATCAGGGCC TGGCTCACTG AGATTTCATGA GTATGCCCAG AGGGACGTGG
451 TGATCATGCT GCTAGGCAAC AAGGCGGATA TGAGCAGCGA AAGAGTGATC
501 CGTTCCGAAG ACGGAGAGAC CTTGGCCAGG GAGTACGGTG TTCCCTTCCT
551 GGAGACCAGC GCCAAGACTG GCATGAATGT GGAGTTAGCC TTTCTGGCCA
601 TCGCCAAGGA ACTGAAATAC CGGGCCGGGC ATCAGGCGGA TGAGCCAGC
651 TTCCAGATCC GAGACTATGT AGAGTCCCAG AAGAAGCGCT CCAGCTGCTG
701 CTCCTTCATG TGAATCCAG GGGGCAGAGA GGAGGCTCTG GAGGCACACA
751 GGATGCAGCC TTCCCCCTCC CAGGCCTGGC TTATTCCAAG AGGCTGAGCC
801 AATGGGGAGA AAGATGGAGG ACTCACTGCA CAGCCGCTTC CTAGCAGGGA
851 GCTATACTCC AACTCCTACT TGAGTTCCTG CCGTCTCCCC GCATCCACAG
901 GGAGGGTAAA ACACCTTAGCT TTTATTTTAA TAGTACATAA TTTAATAACA
951 AAAAAGGCGC CTGGATCCCC AAAAAACCGA GGCTGGGAGC TAGTGGCCCT
1001 TTTGGTTTCT AGGAGTTGGG GGGGGGGGCG TCCGTCGTAA GEATAAGAAA
1051 GGTGGTGTTG CTCCAGCTCA GCCCCAGGGG ACACAGATGC ACTTTGGGGG
1101 TGAGGGCAGG TAATGACTCC ATCGCACCCCT CAGTTCAGCT GGACAGAGGC
1151 TCAGGTGACC CCAGCCTTCA CTGTCTCCCG CTCTCCAGGA GCTTATCTTC
1201 GCCCCATCTC CCAAATAAGT GGGCCCTTGT GCTGTGAGGA AGACCAAAGC
1251 CTCAGGGAAG ATAAGAGATA TGGAGATGGG AGGGGGAGGA CAAGGGGCAG
1301 AGAGTAGGGT CTAGCTGGCT ATCTCTGGCC TTAATAACAC CCCCCTGGAG
1351 GCATGCCCCCT TTTCTCCAGC ACACAAGCAC ATTGGGGCAC CTGGAATAT
1401 TGGTTCAGG CTCCTGTTCT CTGGACTTCA GATCCTGGGG GAGCCCCCTC
1451 CCCCCTGAA TCCCTGGCTT AGCTACCTTC CTGCCTGTGC ACCTAAAAAC
1501 CTCAGGTGAG AACTAGGAAA AGAGTTTGT TTTTATTTT TTGAAATGGA
1551 GTCTCGTTCT GTCGCCAGG CTGAGGTGCA GTAGTGCAAT CTCCGCTCAC
1601 TACAACCTCC ACTCCCTGGG GCTCAAGCGA TCCTCCACC TCAGCCGCG
1651 AAGTAGCTGG GACTATAGGT GTGTACCATC ACACCTGGCT AATTTTGTGTA
1701 TTTTTTGTAG ACACAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAATT
1751 CCTGAGCTCA AGCAACCTGC CGGCCTCGGC CTCCCAAAGT ACTGGGATTA
1801 CACGCAGAAG GCACCATGCC CAGGCTAGAT GTGTCTTATC CCAATCCTTT
1851 GGCAGGCATG CAGCTCCACA GCGGATTTCT TCAAGCAGCT GAAGTGTTTA
1901 GCCCTCCTGG GTTAAGAGCC AGATAAGGAG AAATCCCTTT CTTAGGTTTG
1951 GAATGTGTTG TGAAAAAAA GAGAAATCCC TGGCTCCTGT AGCTGGTGGG
2001 AGACAAGATT AAGCAAAACCT CCCCTGACAT GTATCCCTTT GACCCAAGC
2051 TCTGCCTCCT CCCTGACCAC CCATGCCCTT TCCTTTAACT TCTCAAACAG
2101 ATACCAGGGC CTAAACTGCT TTACCTCCCC TCCTACTGAG TCAGGTTAGG
2151 TGGTGGGAGG TCACCCATTT CCGAGTTAAA CCAATGCAAT ATGAGTAAAA
2201 CAAAGTCATG TGGGTATGTC TGGGGTAGAG AGAGGGGTAG CAAGTTCATG
2251 TGTCTCCTT GGTACATAT CTCCCAAAGC TCTGATCCCT GCCATGGGAA
2301 GTGGACAGGA AACATGAGGT CATGACCTGC AGGCATCTTT ACTGCAGCTC
2351 TGCCGGCCTG GAGGGGGAGA GGGGGAGGAA GAAGTATGCG CTGCACATTT
2401 CTGAGGCTAC TGCATTGCT TTCAAGGCAG AAATCTTGCT CTGAGCAGTC
2451 AGCGGCTCCA GTTTGGGCCC GATAAGGAAG TTCTCCGTGG CCTCCCTCAG
2501 GCAGAGCAGG GAGGAGCTG ACATTGCCAG TCTCTTCTGG GGCCCAAGGC
2551 AGGTTGCAGG AGATCCAATC CCATAGACAG CTCTGGGCCT CTTGCATTTG
2601 AGTTTTTCAG AATTAACTG CAGTATTTTG GAAAGCAAAA AAAAAAAAAA
2651 AAAAAAAAAA AAAAAAAAAA AAAA (SEQ ID NO:1)
```

FEATURES:

5'UTR: 1-41
Start Codon: 42
Stop Codon: 711
3'UTR: 714

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FIGURE 1A



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Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 103000001517087 /altid=gi 10946770 /def=ref NP_067386.1 RA...	425	e-117
CRA 1000682330460 /altid=gi 7657492 /def=ref NP_055168.1 RAB26...	297	4e-79
CRA 18000004977238 /altid=gi 1710022 /def=sp P51156 RB26_RAT RA...	294	3e-78
CRA 18000005013109 /altid=gi 1083775 /def=pir JC2528 GTP-bindi...	293	7e-78
CRA 89000000198627 /altid=gi 7296421 /def=gb AAF51708.1 (AE003...	273	9e-72
CRA 18000005076419 /altid=gi 7438397 /def=pir T15123 hypotheti...	207	4e-52
CRA 18000004912300 /altid=gi 134236 /def=sp P20791 SAS2_DICDI G...	203	7e-51
CRA 98000043536338 /altid=gi 12963499 /def=ref NP_075615.1 cel...	203	9e-51
CRA 18000004929618 /altid=gi 131798 /def=sp P24407 RAB8_HUMAN R...	202	1e-50
CRA 18000004952869 /altid=gi 131848 /def=sp P22128 RAB8_DISOM R...	202	2e-50
CRA 18000005221564 /altid=gi 4586580 /def=dbj BAA76422.1 (AB02...	202	2e-50

BLAST dbEST hits:

	Score	E
gi 13033710 /dataset=dbest /taxon=960...	1318	0.0
gi 12785775 /dataset=dbest /taxon=960...	1316	0.0
gi 12904236 /dataset=dbest /taxon=960...	1035	0.0
gi 9093496 /dataset=dbest /taxon=9606...	694	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|13033710 prostate
gi|12785775 brain
gi|12904236 T cells from T cell leukemia
gi|9093496 leukopheresis

From tissue screening panels:

leukocyte

FIGURE 1B



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1 MTGTPGAVAT RDGEAPERSP PCSPSYDLTG KVMLLGDTGV GKTCFLIQFK
51 DGAFLSGTFI ATVGIDFRNK VVTVDGVRVK LQIWDTAGQE RFRSVTHAYY
101 RDAQALLLLY DITNKSSFDN IRAWLTEIHE YAQRDVVIML LGNKADMSSE
151 RVIRSEDGET LAREYGV PFL ETSAKTGMNV ELAFLAIAKE LKYRAGHQAD
201 EPSFQIRDYV ESQKKRSSCC SFM (SEQ ID NO:2)

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FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

114-117 NKSS (SEQ ID NO:5)

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

1 214-217 KKRS (SEQ ID NO:6)
2 215-218 KRSS (SEQ ID NO:7)

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 5

1 29-31 TGK
2 113-115 TNK
3 149-151 SER
4 173-175 SAK
5 212-214 SQK

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

116-119 SSFD (SEQ ID NO:8)

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 5

1 3-8 GTPGAV (SEQ ID NO:9)
2 6-11 GAVATR (SEQ ID NO:10)
3 39-44 GVGKTC (SEQ ID NO:11)
4 52-57 GAFLSG (SEQ ID NO:12)
5 57-62 GTFIAT (SEQ ID NO:13)

[6] PDOC00017 PS00017 ATP_GTP_A
ATP/GTP-binding site motif A (P-loop)

36-43 GDTGVGKT (SEQ ID NO:14)

[7] PDOC00579 PS00675 SIGMA54_INTERACT_1
Sigma-54 interaction domain ATP-binding region A signature

32-45 VMLLGDTGVGKTCF (SEQ ID NO:15)

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	48	68	0.715	Putative

FIGURE 2A



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BLAST Alignment to Top Hit:

>CRA|103000001517087 /altid=gi|10946770 /def=ref|NP_067386.1| RAB37,
member of RAS oncogene family; GTPase Rab37 [Mus
musculus] /org=Mus musculus /taxon=10090 /dataset=nraa
/length=223
Length = 223

Score = 425 bits (1081), Expect = e-117
Identities = 209/223 (93%), Positives = 215/223 (95%)
Frame = +3

Query: 42 MTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLLGDTGVGKTCFLIQFKDGAFLSGTFI 221
MTGTPGA DGEAPERSPP SP+YDLTGKVMLLGD+GVGKTCFLIQFKDGAFLSGTFI
Sbjct: 1 MTGTPGAATAGDGEAPERSPPFPSPNYDLTGKVMLLGDSGVGKTCFLIQFKDGAFLSGTFI 60

Query: 222 ATVGIDFRNKVVTVDGVRVKLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDN 401
ATVGIDFRNKVVTVDG RVKLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITN+SSFDN
Sbjct: 61 ATVGIDFRNKVVTVDGARVKLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNQSSFDN 120

Query: 402 IRAWLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGVPPFLETSAKTGMNV 581
IRAWLTEIHEYAQRDVVIMLLGNKAD+SSERVIRSEDGETLAREYGVPP+ETSAKTGMNV
Sbjct: 121 IRAWLTEIHEYAQRDVVIMLLGNKADVSSERVIRSEDGETLAREYGVPPFMETSAKTGMNV 180

Query: 582 ELAFLAIAKELKYRAGHQADEPSFQIRDYVESQKKRSSCCSFM 710 (SEQ ID NO:2)
ELAFLAIAKELKYRAG Q DEPSFQIRDYVESQKKRSSCCSF+
Sbjct: 181 ELAFLAIAKELKYRAGRQPDEPSFQIRDYVESQKKRSSCCSFV 223 (SEQ ID NO:4)

Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF00071	Ras family	306.9	8.4e-90	1
CE00060	CE00060 rab_ras_like	213.3	3.7e-60	1
PF01142	Uncharacterized protein family UPF0024	2.6	3.4	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00060	1/1	31	191 ..	25	193 ..	213.3	3.7e-60
PF01142	1/1	185	201 ..	444	462 .]	2.6	3.4
PF00071	1/1	31	223 .]	1	198 []	306.9	8.4e-90

FIGURE 2B



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1 AGGGGAGAGA AAAGACCGCA TACCAGGCCA GGTGCGGTGG CTCACGCTTG
51 TAATCCCAGC AATTTTGAAG GCCAAGGCAG GCGTATCGCC TGAGGTCAGC
101 AGTTCCAAAC CAGCCTGTCC AACATGGTGA AGTTCTCTAC TAAGAATACA
151 AAAATTACCC AGGCGTGGTG GCGTGACCTT GTAGTCCCAG CTGTCCAGAG
201 GGCTGAGGCA GGAGAAATGC TTGAACCTGG GAGGCAGAGG CTGCAATGCG
251 CCAAGATCCC GCCACTGCAC TCCAGCCTGG GCGACAGAGT GAGACTCCGT
301 CTCCGGGAGC CCACGGCATT GAGCAAACCT CGGCATTATT TGCAGCAAGA
351 GCCTCTGGCA TCCAAATAGC AACCAACACC ACGCCTCTGT AGTGTGCTGC
401 GCAGCCTCCA CACTCGAGTC TGAGGCTCCC TGTTTGAGTC CCGCCCTATG
451 CCCAGCTGAG GTTATAGCAC GCTCACCTCC AGAAGAGGTA ACCCAAGCTC
501 TTTACTCTAC TGGAGATCAC CTCTGTCCCC ACTCTGGGCG CTTCTCCCAG
551 CTGACAGAAA ATACCTCCAG CTGATGTGAG AAAATACAGG GCTGGAGGCT
601 GGCGTACAAA GTCAGTCCCC ACAGGCCTAT GGTGGCCCAT AAGCCACGTC
651 TACCCCTGCT CCTCACCTCC ACACCTAAGT TAAGAAATTG AGGCCGGGCG
701 CAGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAGGCTG AGGTGGGCGG
751 ACCGCTGCA CACTCGAATT TGAGACCAGC TTGGCCAACA TGGCAAAACC
801 CCGTCTCTAC TAAAAATACA AAAAGAAAAA ATAGCCGGGC CTGATGTGCG
851 GCACCTGTAA TCCCAGCTAC TCCGGGAGAC TGAGGCGGGA GTATAGCTTG
901 AACCCGGGAA GCAAAGGTTG CAGTGAGGCG AGATCGCACC ACTGCACTCC
951 AGGCTGGGCG ACAGAGTGAG ACTCTGTCTG AAAAAAAAAA AAAGTGCAGG
1001 TACCCCTCTC CAGCTCTCCC CTCCCTACAC ATCCCTCAAA CCGTCCCGCT
1051 GTAATGCACC CGCCCTGTTC CTTGGTAACT TGAAGCTGCT TATAGAATGT
1101 GGAGATGGGG GTAATTGAAA GGTCGGCCCA GGCCACAGAG CCCCTGAGCT
1151 CTGCTACCGG CAACCCAGC TGCACTCCCC ACTCTCTGTC ACCAGGAGCT
1201 GCCGGGTGCC TGGGATATCC TGGCAGCTCT GCTCAAAATG ATCTACGACT
1251 TCATGAATTT ATTTGGCTCC TCCTCGGGGC CAGGGTGAGT GTCATGGGTT
1301 AATAAGGCCG GCCCCGCTT CAGGAGCGGT CCACTGGGAG ATGTGTGCTG
1351 CGCAGCCCTC TTGCGAAAGC TCTCCCTGCG TGGGACATTG TGGGCACAAC
1401 CAACAGGCCG GGGGAAATGA GAGGTGATCC ATACTAAAGG GTCAAAGTCC
1451 CCGCACCAGG CAGAGGCCCC AAAACACCGC AGCGTACATG TGCTGCAAGG
1501 CGAGTACGGG TTGGTAAACA AAATATATT CAGATGAGCT CGGGCCGGGT
1551 GACTTAACAG ATGAGGAAGT GTCTCGGGGC CATCGGCGGA GGCGCAGCCC
1601 AGGGGTCCCC AGCTCCCCGC CTCGCCACCT GGGGACAGCC CACGGCCCGG
1651 GGCTCGGGCG CCGCCTGCTG TCGCGGTGCG CAGCGACTAC GGGAACCTTT
1701 CCGCAGCAGA CGGGTCCCC GCGGCCGCT CCCCAGGGG CAAGCAAGCG
1751 ACCACAGGGG ACCGGTCCCG GGGCTGGATG TGGCTCATGT CCGAAGCGCA
1801 CGGAGCCGAG CCGGTGTTGC TCAGGGAGGC TGCCCGCCCC TTCACGCAGA
1851 CCCTGCGGCT CTGCGTGCCC TCAGGGAACA GCAAGGTCCG AGCCGGTGTC
1901 GTCGAGGGGG CGACGGGACG GAGGGAGGAG CCTGAGGGGT CCCGTCGAG
1951 GGAGGGGAGG AGTGGGCGGG GCGGGGTGG GGGCCGTTCC CGCGCTCTCC
2001 TTCGCCTGCG GGCCGGCACT GCTCACCTCT CGTCCAGGGA CATGACGGGC
2051 ACGCCAGGCG CGGTGGCAC CCGGGATGCG GAGGCCCCG AGCGCTCCCC
2101 GCCCTGCAGT CCGAGTACG ACCTCACGGG CAAGGTGGGT GGGCCTCTTC
2151 CGTGAGACCC CCGCCCTCCT CGGCGTAGC CCCTTCTTGG CTGCGTCTGG
2201 GTTGGACTCA GCCCTTCCCC CAGGCAGCTG CGTCTCCAG AGGAGGGAGG
2251 GAGAGAGGGT CAGGACACAG CCTCTGGGGC CGTCCCAGC TCTAGGTGTC
2301 TCTGCTGGCT TGGTGGGGGC GGGTCGCGGA AGATCGCAA AACTGAGTGA
2351 TCCCCCGGCC GGCCCCAATC CAGTTCTCTT CTGCCAAGT CTGGCAAATA
2401 TGAGCCCCCG GGAGCCCATG CTTCTTGGTG AGGGTTAAGC GCGCAACTCT
2451 CGGGGCTCAG GCTGGGAAGG GCTGGGAGAT GGGGACCGAA CGGAGACTCG
2501 GAGAGGACGT CCCCTGCTGG CAGAGGAACT GGCCTTAATG CCATTTTCCG
2551 AGCTAAGCTC TTAGTTGAGA TCTGACATCC AGGTTTAAGG CCTGATGTCC
2601 CCCAGCTGCT CCCCTCCCAT TCCACCCGCT GGAGGCACTG CCTCCCACCT
2651 TCCTCCCTGC AGTCGGAAGC CGCTCCTCCC AGAAGGATGT TGCCAGCCGG
2701 CCTGCAAGT ACTTGGGAAT TTTTCGAACC TGAGAAAGAT TTCAGTGGTT
2751 GGTCTTTGCG ATCCCCCACT TGAGAGAGCT CCAGGGCTGC TCTCTGGGGC
2801 TTGCTCCCTC TACAGGGGTG TCCTGTATGG AAACAGGTAG GGACAGCAGT
2851 GGAAGTGTCT GTCGCTTCC ATCTGTGTCC TTGGAGTGAG CGGGTACCAG
2901 AAAGTGAAG AACTGCTGAG GGAGCCTAGA GCTTCCACTC TTCCTCTGCA
2951 GGGTTGGGGA TGGAGTGAGG GCTGTCTTGG ATTCCGCTGC ATGGCCTTGA
3001 AGGAGACCTG CCTCTCTCTG GGCTCGGTT TCCTCCCCGA CACCAGGGCT
3051 CACCCTTGCT GGGAGCCTCA GCCTCCACCC CAGTGTTCG GGGGAAGCCA
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FIGURE 3A



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3101	CCCTGCAAGT	CATCCGCCCA	GAGCCGTGA	GATAGGCCTC	CTGTGTGGGC
3151	TTGTGGCAGG	AAATGGGCCC	CTGCACCTC	GGAGAGGAGG	AGCTGTGTGT
3201	GGCCAGGCCC	CAGGCTGAGG	GGGACTGCCT	GACCTTGTGT	CCCTGCAAAC
3251	CAGCTGGGTT	GTTTGCCTAG	GAGGTGGCCA	GGCTAGGCAG	CTGTTTGTGT
3301	TTGGTGGAAAT	CACCGAGCTG	GGTGGGTAGC	TGGCATCGTT	TGCTCAAGGC
3351	AGCTGTGATC	TGTAAAGTAC	ACAAAGACTG	GCCCTCCCTC	CCTCCTTCCT
3401	GCTCCAGGGC	TGGGACCCAG	GAGCCAGGGA	GGAGTGCAGG	CTCCAGAAAG
3451	CTCCTATGCC	CCACCCCTTC	ATCTGTTCCC	TGGCCAAGCG	GCATTGGCCG
3501	GAGAGTTGGT	CCCCAGCCTC	CCCGGGCCTG	CCCCAGGGGA	GTGAGTCCAG
3551	GACCCTCTGA	GAAAGCCTGG	CAGGAGCTCC	TTGGACCAGA	CTAGGGGTGA
3601	TGTGGCCAC	AGGCAGACAG	TTCCACCCT	GGGCCACTCT	TCCCTGGGTC
3651	TTAGGTGATT	CACCACGATG	ATGGGCCCTA	GCCATTAACA	GACTCTAGAA
3701	ATACCTCAA	GACATTATCC	CTCCTCCTTC	TACCCACTAT	GGAAACCATG
3751	CCACAGAAAG	GTTAAGGAAT	CTTCCTAAAG	TCACACAGTA	GGCCATTTAC
3801	AAATCAAGAC	TACCCCTTCT	TACCCCTTCT	GCTCAGCCAC	CCCTGCCTCT
3851	CCACCAGAGT	TAATAATGC	CAGTACCCCA	TGCCCACAAC	AGGAATGCCT
3901	TTGGGCTCCA	CTGTCAATTT	CAGAGCCTCA	AAAATAATTC	AAACCTAGTC
3951	CCTGCTTAAC	CCATTAAGCC	ACCTAACCAG	CAGCTGGGAA	ATTCCAGCAT
4001	TGGATCTAGA	CCCCTGTAT	CCAAGATTGG	AGAACAGTGG	GACAAAGTGC
4051	TCCTCTCCAC	CATTCTGCG	TGTCCCTGGG	GAAGATGAGC	AGAGCAGAGC
4101	CAGACAGTAA	AGGAGAGGGC	CACGCCCCCT	CCACAGGTTA	CCCTGTTGGT
4151	ACTCCTGCCC	GCACTACCCA	CAGCAACCCC	GGGATGCCGA	TCTGCAGCCA
4201	CATGTCCCAT	GTGGGAGGTT	TCTGCTGAAA	GAACCTCCAA	CTACACATCT
4251	CCCCACTTCA	GTATAAATTT	CAACCTTCCC	TAATTCATGC	AACCTTTTTT
4301	TTTTTTTTTT	TTTTTTGAGA	CAGAGTGTG	CTCTGTCAAC	GAGGCTGGAG
4351	TTCACTGATG	CAATCTCGGC	TCACCTGCAAC	CTCTACCTCC	TGGGTTCAAG
4401	CTATTCTCCT	GTCTCCGCCT	CCCAAGTAAC	TGGGACTACA	GGCGTGTGCC
4451	ACCACTCCTG	GCTAGTTTTT	TGTATTTTTA	GTAGAGATGG	GGTTTCACTT
4501	TGTTGGTCTG	GCTGGTCTCA	AACTCCCAAC	TCAGGTGATC	CGTCCACTTG
4551	GGCACCCAAA	ATGNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
4601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
4651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
4701	NNNNNNNNNN	NNNNNNNNNN	TTCAAGTACC	AGCCTGGCCA	ACATGGTAGA
4751	AACCCCGTCT	CTACTAAAAA	TAAAAAATTA	GCCAGGCGAG	GTGGTGCATG
4801	CCTATAATCC	GAGTACTTCA	GGTAGGCTGA	GGCAGGAGAA	TCATTTAAAC
4851	CTGGGAGGTG	GAGGTTGTGG	TGAGCCAAGA	TCTCGCCATT	GCACTCCAGC
4901	CTGGGCAACA	AGAGCAAAAC	TCCGTCTCAA	AAAAAAAAG	AAAGAAAGAA
4951	AGAAAGAAAC	TTCCAAATAA	ATGTTGTGAC	ACAAAAAAA	AAACCCAAAC
5001	AATATTCAAT	ATAGAGTATG	CAAATGACCA	TGCCCCACCC	CCAGCAGATT
5051	CTGATAGACT	CCCTTGGGTG	GGAATCCTTG	TCCAATATAT	TGACACTTCC
5101	CTTTCCTGTC	AGTATAGCCC	AGCCCATGCG	TGTACTCAGC	AGCGGACGAT
5151	GGATGACACA	AGTACACAGA	GGGACGGAAT	CCCTGCATGG	TGTGGCTATG
5201	GGCAAATGTG	GCCACTGTCT	AGATTGTGCA	AATGTGGTGG	TTCTCTGGGG
5251	CCACAGAGCA	CACTTGGGGA	CCTGTTTCATG	GTGAGGTCTC	AACTCCGGCC
5301	TCTAGGAAGT	TGAATGAGGA	CAGGAGGGTC	AGAGGGAGAG	CCTAGGAGGC
5351	TGAGCCAAGG	AGCGTGGAGA	GGAGAGACAG	GGTGAAGGTG	GCGGCTGGCT
5401	TTCTGGAAGC	AGGTGGCCTT	TGGTGGCGTC	AGCATTCGTG	CCAGCCCCCT
5451	CTTCTCTGAT	CCTCTCCATG	TGTCTCTCTC	CTGGAATCCC	AGAAGCTGCC
5501	CCTGACTCCC	CATTAAGTGC	CTCTGCCCTT	ACCCCTAGG	TGATGCTTCT
5551	GGGAGACACA	GGCGTCGGCA	AAACATGTTT	CCTGATCCAA	TTCAAAGACG
5601	GGGCCTTCCT	GTCCGGAACC	TTCATAGCCA	CCGTCGGCAT	AGACTTCAGG
5651	GTGAGGTGGC	TGCAGGCACT	TGCTTCCAGC	AGAGAGCCAG	GGCTGTGGCT
5701	CAGGCATGGG	GGGGTTGCCC	CCACCTTGCT	CACCCTGGCT	CCCAGGGACT
5751	CCCGAGGCTC	ATGCTGGGAG	GGCACACAAC	CCGCTCCCCC	AAGACCACAG
5801	AGGTGGCCGG	GTCAAAGGAG	ACTGGGCAAG	GTTGGCTCCT	TGCCCAACTA
5851	TAGGATGCAA	AAAAATGAGA	CTGAGTCTTC	GATTCCAGCT	CCATTCTCTG
5901	GGGACTTCTC	CCAAGCAGAG	CAGCCGCAGG	CACGGCATAA	GCTGAATATC
5951	TTGGCCACAC	GAGCCCCTGC	TCATTGCTCT	CCTACCTGGG	CCCCTTTGGA
6001	AAGGCCTCAA	AGGTCAATCA	GTCTTTCTGG	AGTTCCCAGA	AAGCACAGCC
6051	CTGCACTGGG	TTTAAGAGCT	GGGCTTGGGC	CAGGCATGGT	GGCTCTTGCC
6101	TGTATTCCCA	GCACCTTGGG	AGGCCGAAGC	GGTCAGATCA	CAAGGTCAGG
6151	AGTTTGAGAC	CAGCCTGGCC	AACATGGTGA	AACCCCGTCT	CTACTAAAAA

FIGURE 3B



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6201 TACAAAAAATT AGCCAGGTGT AGTGGCACGC TCCTGCAGTC CCAGCTACTC
6251 GGGAGGCTGA GGCAGGAGAA TCGCTCAAAT CCGGGTGGTG GAGGTTGCAG
6301 TGAGCTGAGA TCGCGCCACT GCACTCCAGC CTGGGCAACA AAGTGAGACT
6351 GCGTCTCAGA AAAAAAAAAA AAAAAAGAGC TGGGCTGGCC ATGTTGGGAG
6401 ACAGCAGCTC ACCAGGGACC CTCCCTCTCA CCTTGACGAC TCCATCTTAC
6451 AAATCTGCAT CAGGGATGCT AGACGCTGCA CACCTGAAGT GTTCAATAGA
6501 GAAAAGGTCT CACCCTGGCA GGTGGGGCTC TACAGCTTCA AGCAGGCAGA
6551 AAGCGAACAC TTCTTCACT AGAGAATTAG TGGGCAGTGA AAGAAAAGGT
6601 GCTGCTGCAG ATGTAGCCTC AGGTCCCCAG GATGCAGCA AACACCCCAT
6651 CTCCAGGGGC TCGGTCACAG TCCCAAGGCT AGGCTCCAGG AGAGGGAGAC
6701 CGAAGTGGGG AAAGGGCAGG GCCTCCAGCA GCAACCAGCC CTCCAGCCCT
6751 GGGCTGCCTG ATCCCTGGAG AGAGCCAGGA TGTTTCTCAG GCTCCTCTTG
6801 CCCTGCTGTT GTGAGAAGGC AGTTACAGTC CTCAGAAGGG ACGACTCCAC
6851 AGTGGAGGTG TCTGGGTATG GGGTTCCTGC TGCCCTGATG GTATGATCTG
6901 GCTGGAGACG TTTCTGGGGC TCACTGCACC CACTTAGGAC CTGGAGAGGG
6951 AACAAGAGAG GACGTCTGCA GAGCTGAGGA GCCACATGAC TCCTGCCTC
7001 CCATCCTCTG CTTTTTCTC TTTCAGAACA AGGTGGTGAC TGTGGATGGC
7051 GTGAGAGTGA AGCTGCAGGT GAGACCAGAG GCTGGAGTTG GGGAGGGAGG
7101 ATGGAGGACC TGCCCTTCCCT TCTCACCCCTG AACCACAGGA GGCCTGCAGC
7151 CCTGCCCTCC GCCTGGGGCA ATTTCTGTG GGGCCACGG GAGGAAATGG
7201 CTTTTGTTTA TTGTACATCT GCAGAAAAAG CAGTTCCTCAG GCACCTCTC
7251 ATCTATGAAC AGCAGCTCCA AATGCCTTCA GACAAGCTTA GCCTCCATCC
7301 ATCTCCTCCC CAGTTGCCAG GGCTTTATCT GCTCTTAGGA GATTGGACAT
7351 CCCCACCCCC TGAGCTAGGG GAGAGGAGAA GATTCTTTTT TTTTCTTTTC
7401 TTTTCTTTTT TTTTTTGAGA TGGAGTCTCG CTCTGTCGCC CAGGCTGGAG
7451 TGCAGTGGCA CAATCTCGGC TCACTGCAAC CTCTGCCTCC CAGGTTTAAG
7501 AGATTCTCCT GCCTCAGCCT CCTGAGTAGC TGAGACTACA GGTGCATGCC
7551 ACCACACCTG GATAATTTT GTAGAGACGG GGTTCCTACTG
7601 TGTTAGCCAG GATGGTCTGG ATCTCCTGAC CTCGTGATCC GCCTGCCTCG
7651 GCCTCCCAAA GTGCTGGGAT TACAGGTGTA AGCCACCGCG CTCGGCTGAG
7701 GAGATGATTT TGAACGAGCT TGAGAAATCA GTAAGTCTA CTGTCCAGGT
7751 CATTGGATGC TCAGGGGCTC ATGAGAACTT AAAGAAGAAA ACAGCCCCAC
7801 CTTCCACAG ATATCTCATA CAACAAAGCA GGCTGCTCC ACCCAGCACA
7851 TTCCTTGAC CTGCCTCCTT CTGACCATT CTCCATCCCA TCCCTTCCCA
7901 GATCTGGGAC ACCGCTGGGC AGGAACGGTT CCGAAGCGTC ACCCATGCTT
7951 ATTACAGAGA TGCTCAGGGT GAGTCCCTCG CACCCTCCAA CCCCTACCCC
8001 AGCCCCCTGG TAGCATCCGT GCTGCTGCCT AAGTCCCTC TGTGATCCTC
8051 TCCCTCCAG CTTGCTTCT GCTGTATGAC ATCACCACA AATCTTCTTT
8101 CGACAACATC AGGGTAGGTC CTCCCTTCCC CTGACTCCCA CCCATAAGCA
8151 GCCAAGGCAA GGTCTATGCA GGCTGGGGTT GCTTCTGCC CTGTGGAAAG
8201 CGGGTGGAGC GTGGAGTCCT CCTGCCCTCT GAAAAACACC TACTTGTGAC
8251 TCAGAAAGTCA TATCTGTGC TTTGTATTG GTGGCCATGT GGGCATGAAG
8301 GCCAAGCAGG CTGTTGTGAC CCTGTGCCAC CTGCATAGCC CTCACTGTGA
8351 TTCACGAGTG TGTTTCGTGA CAAAGTGTTC AGAACAGCCC CCACTCCACC
8401 CTGGATAAAT ATCCACAGAG ACCAAGGGAA AAACACAACC AGAAAAGTCC
8451 ACACATACAT CCAGGGCAAG TTGCAAGAAA GTGACTCAGT CAGACAGAGT
8501 GAGTGGTTGT ATCCTCACAA CCAACTATT ATAGAGACAA AAATTTGATA
8551 AATTCAAGCA CCAATTTGT TCACGACATT GTATAGGTTT CATGAATCCC
8601 CTGACCTCAA GGACAGTTTG CTGATAAGCA AACTAGGAGA ATAAAACGTT
8651 TATATAGAAA GAGGAAAAATC CATGGCACTC ATACTCCTAC CTCCAACCCC
8701 ATGCTCATGG CAGACATCAC TAATCAATCA CAGTACTTTT GATCACTGAA
8751 ACCCTTATGT GGTCTTAGAA TCTTTAACAG GACACTCCAA GAAATCACTG
8801 CTGACAGCCA ACTGATTTGT GAGATAAGGT CTCCATGCAT CTGGATCTTC
8851 CATAGAACTG ATAGTTGCAC AGCATAAAAT GGTGAGGGTG GGGCCATTGT
8901 GGGTTGAGCC ACCAAGGAAG GCCATCCAGG CCTGGATGGG CCAGAACAAA
8951 GGTACAGATG AGAGAACGCA CAGGGTATCG TGTTCAAGGT AGTGAGTAAC
9001 TGAGGATAGT CAAACGGAGC AGAAGAAGAA AGGGGCAGCA GGAGGAAGAG
9051 AATGCCAGTC TCGCACGCCC TCTCCACAG GCCTGGCTCA CTGAGATTCA
9101 TGAGTATGCC CAGAGGACG TGGTGATCAT GCTGCTAGGC AACAGGTGA
9151 GTGGCTCCGG GGCAGGGTCA GCCCAGCCCT GCACTTCCTC AGCCCTAGCC
9201 GGCCCCATAA CCACCAAGA ACAGTTATCT AGGCATCCTT CCTGAAAAGG
9251 ACTCTGCAGC CTCCAGCTCA GGGGTCAGAC ATATCTGGAG GCTTCTGCC

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FIGURE 3C



Docket No.: CL001187
Serial No.: 09/817,199
Inventors: SHAO, Wei et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

9301 ATCCCATCTG CCCCTTCCAG GGAAAGTCCA AGTTGTTGCC TGAGAAATCA
9351 AGGGGTGCCC AGTTCTCAGC CCCCATTAGA GCAGAGTGAA CAGGGTCCCA
9401 GGTCAGGGGC TAAGAGTGCA AAGGGTTAGC CCCAAGTCTG GTCCTATTCC
9451 AAGACCCCTT ACCAAAGGTG AGATCCCAGA GCTGGGAGCT AACTGGGCA
9501 GAAACCCCTG CCCAGGCCA ATCACACCTG CCTGCAGTCC CTTGGGCCAC
9551 CAGCAGAGGG CAGGCAACGC CTGCTTCTGG GGCAAAATAT GGGCCCGCTG
9601 GGGCGGAGGC CTCCTTCCCC AGAGTGACCC ATTTGGGCTT GACAGGCGGA
9651 TATGAGCAGC GAAAGAGTGA TCCGTTCCGA AGACGGAGAG ACCTTGGCCA
9701 GGGTAAGTGA TTGTCTGTGG GACAGGGTGA AGGGTGGGGG CAACCCGACG
9751 CTGGCCCTGA GGACACTCTC TCCCGGGCAG GAGTACGGTG TTCCCTTCTT
9801 GGAGACCAGC GCCAAGACTG GCATGAATGT GGAGTTAGCC TTTCTGGCCA
9851 TCGCCAAGTG AGAGCTGGGC AGGGAAGGGA AGTGTGCGGG GCAGGGCGGC
9901 ACACTCCAGG AATCCAGTAG GGCCCGGCCC CTGGCCAGC CCCTGGACAC
9951 ACCTGCATTG TGCAGGCTGA GGTCCATTG CTCTGGGAGC ACTGGGCCAC
10001 TGGGAGAGGG GAGGGGGCGG CTCAGCTCCT CACCCAGCC CAGCCAGCC
10051 CAGCCAGCC CATGTCTCT TCTTCAAGGG AACTGAAATA CCGGGCCGGG
10101 CATCAGGCGG ATGAGCCAG CTTCCAGATC CGAGACTATG TAGAGTCCCA
10151 GAAGAAGCGC TCCAGCTGCT GCTCCTTCAT GTGAATCCCA GGGGGCAGAG
10201 AGGAGGCTCT GGAGGCACAC AGGATGCAGC CTTCCCCCTC CCAGGCCTGG
10251 CTTATTCCAA GAGGCTGAGC CAATGGGGAG AAAGATGGAG GACTCACTGC
10301 ACAGCCGCTT CCTAGCAGGG AGCTATACTC CAACTCCTAC TTGAGTTCCT
10351 GCGGTCTCCC CGCATCCACA GGGAGGGTAA AACACTTAGC TTTTATTTTA
10401 ATAGTACATA ATTTAATACC AAAAAAGGCG CCTGGATCCC CAAAAACCG
10451 AGGCTGGGAG CTAGTGGCCC TTTTGCTTTC TAGGACTTGG GGGGCCGGCC
10501 CTCCCTCCTA AGCATAACAA AGGTGGTGTG GCTCCAGCTC AGCCCCAGGG
10551 GACACAGATG CACTTTGGGG GTGAGGGCAG GTAATGACTC CATCGACCCC
10601 TCAGTTCAGC TGGACAGAGG CTCAGGTGAC CCCAGCCTTC ACTGTCTCCC
10651 GCTCTCCAGG AGCTTATCTT CGCCCCATCT CCCAAATAAG TGGGCCCTTG
10701 TGCTGTGAGG AAGACCAAG CCTCAGGGAA GATAAGAGAT ATGGAGATGG
10751 GAGGGGGAGG ACAAGGGGCA GAGAGTAGGG TCTAGCTGGC TATCTCTGGC
10801 CTTACTAACA CCCCCCTGGA GGCATGCCCC TTTTCTCCAG CACACAAGCA
10851 CATTGGGGCA CCTGGAATAA TTGGTTCCAG GCTCCTGTTC TCTGGACTTC
10901 AGATCCTGGG GGAGCCCCCTC CCCCCCTGA ATCCCTGGCT TAGTACCTT
10951 CCTGCCTGTG CACCTAAAAA CCTCAGGTCA GAACTAGGAA AAGAGTTTGT
11001 TTTTATTTT TTTGAAATGG AGTCTCGTTC TGTCGCCGAG GCTGAGGTGC
11051 AGTAGTGCAA TTTCCGCTCA CTACAACCTC CACTCCCTGG GGCTCAAGCG
11101 ATCCTCCAC CTCAGCCGCC GAAGTAGCTG GGAATATAGG TGTGTACCAT
11151 CACACCTGGC TAATTTTTGT ATTTTTTGTG GACACAGGGT TTCGCCATGT
11201 TGCCCAGGCT GGTCTTGAAT TCCTGAGCTC AAGCAACCTG CCGGCCTCGG
11251 CCTCCCAAAG TACTGGGATT ACACGCAGAA GGCACCATGC CCAGGCTAGA
11301 TGTGCTTAT CCCAATCCTT TGGCAGGCAT GCAGCTCCAC AGGCGATTTC
11351 TTCAAGCAGC TGAAGTGTTT AGCCCTCCTG GGTTAAGAGC CAGATAAGGA
11401 GAAATCCCTT TCCTAGGTTT GGAATGTGTT GTGAAAAAAA AGAGAAATCC
11451 CTGGCTCCTG GAGCTGGTGG GAGACAAGAT TAAGCAAACC TCCCCTGACA
11501 TGTATCCCTT TGACCCCAAG CTCTGCCTCC TCCCTGACCA CCCATGCCCT
11551 TTCCTTTAAC TTCTCAAACA GATACCAGGG CCTAAACTGC TTTACCTCCC
11601 CTCCTACTGA GTCAGGTTAG GTGGTGGGAG GTCACCCATT TCCGAGTTAA
11651 ACCAATGCAA TATGAGTAAA ACAAAGTCAT GTGGGTATGT CTGGGGTAGA
11701 GAGAGGGGTA GCAAGTTCAT GTGTCTCCTT TGGTCACATA TCTCCCAAAG
11751 CTCTGATCCC TGCCATGGGA AGTGGACAGG AAACATGAGG TCATGACCTG
11801 CAGGCATCTT TACTGCAGCT CTGCCGGCCT GGAGGGGGAG AGGGGGAGGA
11851 AGAAGTATGC GCTGCACATT TCTGAGGCTA CTGCATTTGC TTTCAAGGCA
11901 GAAATCTTGC TCTGAGCAGT CAGCGGCTCC AGTTTGGGCC CGATAAGGAA
11951 GTTCTCCGTG GCCTCCCTCA GGCAGAGCAG GGAGGAGGCT GACATTGCCA
12001 GTCTCTTCTG GGGCCCAAGG CAGGTTGCAG GGATCCCAAT CCCATAGACA
12051 GCTCTGGGCC TCTTGCAATT GAGTTTTTCA GAATTAAACT GCAGTATTTT
12101 GGAAAGCACA TCCTGTCCAC TGTTTCTTTG AAGTGAGTGG GGGGGGGGGG
12151 TCTTGTTGAA GGAATTGTCA TTTACTGCCA AAATCATTCC ATCCTCCTTC
12201 CTCAGTGTCT GTCCTCAGAT GGTGAGCTCC CCGCTCAACA GACTGTCTCC
12251 CGCCTCTGTG ACCAGCCTCT CTTTGGCAAG AGGGAGCTAG AAGGCTTTAC
12301 AGTCCTAATC ATTTTCTGTG TGGAAAAAAA AAAAAAAAC CAAGGCTCCT
12351 TTCCCTGTGG CGTGTACCCA GAGGTTGATT ACCTGAGTCT GTCCTGCCTC

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FIGURE 3D



Docket No.: CL001187
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Inventors: SHAO, Wei et al.

Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

```
12401 TCCCCACCCC ACCTCCCTAG CCAAACGCTG CTGCCAAAGC CCACGCTATT
12451 GCCCTAGATG GCCTGTCTTC AGCGGGCTGC CCCTCGAGGT CCCAGGCTCT
12501 CCGCGGAGCC CTCACCTTCC CAGCAGGGAT CAGAACCCTGC ACTCCTCTAT
12551 GCGAGTCCTG GGACAGCACA AAGTGGATTA GGGTTAGGGT TCCCACAAAC
12601 GGAAAAATGT TATTCAAACA ACTCTGTAGG GTCCGAGGAG GCCCTCCGTC
12651 TTAATTCTCG AGACTGACCG GCCCTCGCTG CCCCAGAGCGG GAGCAGTTGC
12701 CCCGGCAACA GCCGCTCCCT CTCAACTGGA GCTGCACCCA GGCTTTGGCT
12751 AAAGGCTGTT AAAACGTTGG CCAGGTGCGG AGGCTCACGT CTGTAATCCC
12801 AGGGCGGATC ACCTGAGGTC AGGAGTTTGA AACCATCCTG GCCAACATGG
12851 CGAAATTTTC TCTCTACTAA AAATACAAAA ATTAGCGGGG CGTGGTGGTG
12901 CGCGCCTGTA ACCCCAGCTG CTCGGGAGGC TGAGGCAGGG GAATCGCTTG
12951 AACC CGGGAG GCGGAGGTTG CAGTGATCCG AGATCGCGCC ACGGCAGTCC
13001 AGCCTGGGCG ACAGAGCGAG ACTCCGTCTC AAAAAAAAAA AAAAAAGTTA
13051 GGGTCCTTTA CCCGAGGGCC GGCTTTCTCT ACTCCCGGCC ACAGGTAGGG
13101 GAAACCAGGC CGGAGCCGGC GGGCCCACCC GCCCAGAACC GGGAATTCCG
13151 CGAGCCCCGC CCCTGCCACC CCAGCGCCGG CC (SEQ ID NO:3)
```

FEATURES:

Start: 2042
Exon: 2042-2134
Intron: 2135-5539
Exon: 5540-5650
Intron: 5651-7026
Exon: 7027-7068
Intron: 7069-7901
Exon: 7902-7968
Intron: 7969-8060
Exon: 8061-8113
Intron: 8114-9080
Exon: 9081-9146
Intron: 9147-9645
Exon: 9646-9702
Intron: 9703-9780
Exon: 9781-9857
Intron: 9858-10078
Exon: 10079-10181
Stop: 10182

CHROMOSOME MAP POSITION:

Chromosome # 17

ALLELIC VARIANTS (SNPs):

DNA			
Position	Major	Minor	Domain
4259	C	T	Intron
4325	G	T	Intron
4348	G	A	Intron
4924	G	A	Intron
4983	-	A	Intron
6710	A	G	Intron
8624	A	G	Intron
8661	G	A	Intron
11754	T	C	Beyond ORF(3')
11836	A	G	Beyond ORF(3')

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Context:

DNA
Position
4259

ACCCATTAAGCCACCTAACCCAGCAGCTGGGAAATTCAGCATTGGATCTAGACCCCTGTT
ATCCAAGATTGGAGAACAGTGGGACAAAGTGCTCCTCTCCACCATTCTGCGTGTCCCTG
GGGAAGATGAGCAGAGCAGAGCCAGACAGTAAAGGAGAGGGCCACGCCCCCTCCACAGGT
TACCTCCTTGGTACTCCTGCCCGCACTACCCACAGCAACCCCGGATGCCGATCTGCAGC
CACATGTCCCATGTGGGAGGTTTCTGCTGAAAGAACTTCCAACCTACACATCTCCCCACTT
[C, T]
AGTATAAATTTCAACCTTCCCTAATTCATGCAACCTTTTTTTTTTTTTTTTTTTTGGAG
ACAGAGTGTGCTCTGTACCGAGGCTGGAGTTCAGTGATGCAATCTCGGCTCACTGCAA
CCTCTACCTCCTGGGTTCAAGCTATTCTCCTGTCTCCGCTCCCAAGTAACTGGGACTAC
AGGCGTGTGCCACCACTCCTGGCTAGTTTTTTGTATTTTTAGTAGAGATGGGGTTTACC
TTGTTGGTCAGGCTGGTCTCAAACCTCCCAACTCAGGTGATCCGTCCACTTGGGCACCCAA

(SEQ ID

NO:16)

4325

GATTGGAGAACAGTGGGACAAAGTGCTCCTCTCCACCATTCTGCGTGTCCCTGGGGAAG
ATGAGCAGAGCAGAGCCAGACAGTAAAGGAGAGGGCCACGCCCCCTCCACAGGTTACCTC
CTTGGTACTCCTGCCCGCACTACCCACAGCAACCCCGGATGCCGATCTGCAGCCACATG
TCCCATGTGGGAGGTTTCTGCTGAAAGAACTTCCAACCTACACATCTCCCCACTTCAGTAT
AAATTTCAACCTTCCCTAATTCATGCAACCTTTTTTTTTTTTTTTTTTTTGAGACAGA
[G, T]
TGTCGCTCTGTACCGAGGCTGGAGTTCAGTGATGCAATCTCGGCTCACTGCAACCTCTA
CCTCCTGGGTTCAAGCTATTCTCCTGTCTCCGCTCCCAAGTAACTGGGACTACAGGCGT
GTGCCACCACTCCTGGCTAGTTTTTTGTATTTTTAGTAGAGATGGGGTTTACCTTGTG
GTCAGGCTGGTCTCAAACCTCCCAACTCAGGTGATCCGTCCACTTGGGCACCCAAAATG

(SEQ ID

NO:17)

4348

TGCTCCTCTCCACCATTCTGCGTGTCCCTGGGGAAGATGAGCAGAGCAGAGCCAGACAG
TAAAGGAGAGGGCCACGCCCCCTCCACAGGTTACCTCCTTGGTACTCCTGCCCGCACTAC
CCACAGCAACCCCGGATGCCGATCTGCAGCCACATGTCCCATGTGGGAGGTTTCTGCTG
AAAGAACTTCCAACCTACACATCTCCCCACTTCAGTATAAATTTCAACCTTCCCTAATCA
TGCAACCTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTGTGCTCTGTACCGAGGCTG
[G, A]
AGTTCAGTGATGCAATCTCGGCTCACTGCAACCTCTACCTCCTGGGTTCAAGCTATTCTC
CTGTCTCCGCTCCCAAGTAACTGGGACTACAGGCGTGTGCCACCACTCCTGGCTAGTTT
TTTGTATTTTTAGTAGAGATGGGGTTTACCTTGTGGTCAGGCTGGTCTCAAACCTCCA
ACTCAGGTGATCCGTCCACTTGGGCACCCAAAATG

(SEQ ID NO:18)

4924

TTCAAGTACCAGCCTGGCCAACATGGTAGAAACCCCGTCTCTACTAAAAATAAAAAATTA
GCCAGGCGAGGTGGTGCATGCCTATAATCCCAGCTACTCAGGTAGGCTGAGGCAGGAGAA
TCATTTAAACCTGGGAGGTGGAGTTGTGGTGAGCCAAGATCTCGCCATTGCACTCCAGC
CTGGGCAACAAGAGCAAAACTCC
[G, A]
TCTCAAAAAAAAAAAGAAAGAAAGAAAGAAAGAACTTCCAAATAAATGTTGTGACACAA
AAAAAAAAACCCAAACAATATTCAATTATAGAGTATGCAAATGACCATGCCCCACCCCCAG
CAGATTCTGATAGACTCCCTTGGGTGGGAATCCTTGTTCCAATATATTGACACTTCCCTTT
CCTGTGAGTATAGCCAGCCCATGCGTGTACTCACGAGCGGACGATGGATGACACAAGTA
CACAGAGGGACGGAATCCCTGCATGGTGTGGCTATGGGCAAATGTGGCCACTGTCTAGAT

(SEQ ID

NO:19)

4983

TTCAAGTACCAGCCTGGCCAACATGGTAGAAACCCCGTCTCTACTAAAAATAAAAAATTA
GCCAGGCGAGGTGGTGCATGCCTATAATCCCAGCTACTCAGGTAGGCTGAGGCAGGAGAA
TCATTTAAACCTGGGAGGTGGAGTTGTGGTGAGCCAAGATCTCGCCATTGCACTCCAGC
CTGGGCAACAAGAGCAAAACTCCGTCTCAAAAAAAAAAAGAAAGAAAGAAAGAAAGAAAC
TTCCAAATAAATGTTGTGACAC

FIGURE 3F

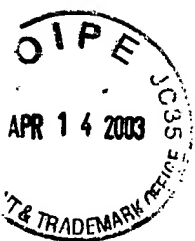


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Serial No.: 09/817,199
Inventors: SHAO, Wei et al.
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[-, A]
AAAAAAAAAACCCAAACAATATTCTATTATAGAGTATGCAAATGACCATGCCCCACCCCA
GCAGATTCTGATAGACTCCCTTGGGTGGGAATCCTTGTCCAATATATTGACACTTCCCTT
TCCTGTCAGTATAGCCAGCCCATGCGTGACTCAGAGCGGACGATGGATGACACAAGT
ACACAGAGGGACGGAATCCCTGCATGGTGTGGCTATGGGCAAATGTGCCCACTGTCTAGA
TTGTGCAAATGTGGTGGTTCTCTGGGGCCACAGAGCACACTTGGGGACCTGTTTCATGGTG (SEQ ID
NO:20)
6710 CACCAGGGACCTCCCTCTCACCTTGACGACTCCATCTTACAAATCTGCATCAGGGATGC
TAGACGCTGCACACCTGAAGTGTTCAATAGAGAAAAGGTCTCACCTGGCAGGTGGGGCT
CTACAGCTTCAAGCAGGCAGAAAGCGAACACTTCTTCACTAGAGAATTAGTGGGCAGCT
AAAGAAAAGGTGCTGCTGCAGATGTAGCCTCAGGTCCCCAGGATGCAGGCAAACACCCCA
TCTCCAGGGGCTCGGTACAGTCCCAAGGCTAGGCTCCAGGAGAGGGAGACCGAAGTGGG
[A, G]
AAAGGCGAGGGCCTCCAGCAGCAACCAGCCCTCCAGCCCTGGGCTGCCTGATCCCTGGAG
AGAGCCAGGATGTTTCTCAGGCTCCTTGGCCCTGCTGTTGTGAGAAGGCAGTTACAGTC
CTCAGAAGGGACGACTCCACAGTGGAGGTGTCTGGGTATGGGGTCTCTGCTGCCCTGATG
GTATGATCTGGCTGGAGACGGTCTGGGGCTCACTGCACCCACTCTAGGCCTGGAGAGGG
AACAGAGAGGACGCTCTGCAGAGCTGAGGAGCCACATGACTCCTGCCTCCCATCCTCTG (SEQ ID
NO:21)
8624 GTGCCACCTGCATAGCCCTCACTGTGATTACGAGTGTGTTTCGTGACAAAGTGTTTCA
ACAGCCCCACTCCACCTGGATAATTATCCACAGAGACCAAGGGAAAAACACAACCAGA
AAAGTCCACACATACATCCAGGGCAAGTTGCAAGAAAGTGACTCAGTCAGACAGAGTGAG
TGGTTGTATCCTCACAACCAAATATTATAGAGACAAAAATTTGATAAATTCAAGCACCA
ATTTTGTTCACGACATTGTATAGGTTTCATGAATCCCTGACCTCAAGGACAGTTTGCTG
[A, G]
TAAGCAAACCTAGGAGAATAAAACGTTTATATAGAAAGAGGAAAAATCCATGGCACTCATA
TCCTACCTCCAACCCCATGCTCATGGCAGACATCACTAATCAATCAGTACTTTTGATC
ACTGAAACCTTATGTGGTCTTAGAATCTTTAACAGGACACTCCAAGAAATCACTGCTGA
CAGCCAACTGATTTGTGAGATAAGGTCTCCATGCATCTGGATCTTCCATAGAAGTATAG
TTGCACAGCATAAAATGGTGAGGGTGGGGCCATTGTGGTTGAGCCACCAAGGAAGGCCA (SEQ ID
NO:22)
8661 TGTTCGTGACAAAGTGTTTCAAGAACGCCCCCACTCCACCTGGATAATTATCCACAGAG
ACCAAGGGAAAAACACAACCAGAAAAGTCCACACATACATCCAGGGCAAGTTGCAAGAAA
GTGACTCAGTCAGACAGAGTGAGTGGTGTATCCTCACAACCAAATATTATAGAGACAA
AAATTTGATAAATTCAAGCACCAATTTGTTTACGACATTGTATAGGTTTCATGAATCCC
CTGACCTCAAGGACAGTTTGCTGATAAGCAAACCTAGGAGAATAAAACGTTTATATAGAAA
[G, A]
AGGAAAATCCATGGCACTCATACTCCTACCTCCAACCCCATGCTCATGGCAGACATCACT
AATCAATCAGTACTTTTGATCACTGAAACCTTATGTGGTCTTAGAATCTTTAACAGG
ACACTCCAAGAAATCACTGCTGACAGCCAACTGATTTGTGAGATAAGGTCTCCATGCATC
TGGATCTTCCATAGAAGTATAGTTGCACAGCATAAAATGGTGAGGGTGGGGCCATTGTG
GGTTGAGCCACCAAGGAAGGCCATCCAGGCCTGGATGGGCCAGAACAAAGGTACAGATGA (SEQ ID
NO:23)
11754 GCTCCTGGAGCTGGTGGGAGACAAGATTAAGCAAACCTCCCCTGACATGTATCCCTTTGA
CCCCAAGCTCTGCCTCCTCCCTGACCACCCATGCCCTTTCCTTTAACTTCTCAAACAGAT
ACCAGGGCCTAAACTGCTTTACCTCCCCTCCTACTGAGTCAGGTTAGGTGGTGGGAGGTC
ACCCATTTCCGAGTTAAACCAATGCAATATGAGTAAACAAAGTCATGTGGGTATGTCTG
GGGTAGAGAGAGGGGTAGCAAGTTTATGTGTCTCCTTGGTTCATATCTCCCAAAGCTC
[T, C]
GATCCCTGCCATGGGAAGTGGACAGGAAACATGAGGTGATGACCTGCAGGCATCTTTACT
GCAGCTCTGCCGCCCTGGAGGGGGAGGGGGAGGAAGAAGTATGCGCTGCACATTTCTG
AGGCTACTGCATTTGCTTTCAAGGCAGAAATCTTGCTCTGAGCAGTCAGCGGCTCCAGTT
TGGGCCCGATAAGGAAGTTCTCCGTGGCCTCCCTCAGGCAGAGCAGGGAGGAGGCTGACA
TTGCCAGTCTCTTCTGGGGCCCAAGGCAGGTTGCAGGAGATCCAATCCCATAGACAGCTC (SEQ ID
NO:24)
11836 GACCACCCATGCCCTTTCCTTTAACTTCTCAAACAGATACCAGGGCCTAAACTGCTTTAC
CTCCCCTCCTACTGAGTCAGGTTAGGTGGTGGGAGGTACCCATTTCCGAGTTAAACCAA

FIGURE 3G



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TGCAATATGAGTAAACAAAGTCATGTGGGTATGTCTGGGGTAGAGAGAGGGGTAGCAAG
TTCATGTGTCCTCCTTGGTCACATATCTCCCAAAGCTCTGATCCCTGCCATGGGAAGTGG
ACAGGAAACATGAGGTCATGACCTGCAGGCATCTTTACTGCAGCTCTGCCGGCCTGGAGG
[A, G]
GGAGAGGGGGAGGAAGAAGTATGCGCTGCACATTTCTGAGGCTACTGCATTTGCTTTCAA
GGCAGAAATCTTGCTCTGAGCAGTCAGCGGCTCCAGTTTGGGCCCCGATAAGGAAGTTCTC
CGTGGCCTCCCTCAGGCAGAGCAGGGAGGAGGCTGACATTGCCAGTCTCTTCTGGGGCCC
AAGGCAGGTTGCAGGAGATCCAATCCCATAGACAGCTCTGGGCCTCTTGCATTTGAGTTT
TTCAGAATTAACTGCAGTATTTTGGAAAGCACATCCTGTCCACTGTTTCTTTGAAGTGA

NO: 25)

(SEQ ID

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FIGURE 3H